Monday, October 1, 2001

Blast 2 Sequences

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program [blastp ▼] Matrix [BLOSUM62 ▼]

Parameters used in BLASTN program only:
Reward for a match: [＿＿＿＿] **Penalty for a mismatch:** [＿＿＿＿＿]
☒ Use Mega BLAST   Strand option [Not Applicable ▼]

Open gap [11] and extension gap [1] penalties
gap x_dropoff [50] expect [10] word size [3] Filter ☑

Sequence 1 Enter accession or GI [DEGP] or download from file [＿＿＿＿＿＿]
or sequence in FASTA format from: [＿＿＿] to: [＿＿＿]

```
tvntprmprnrqqrrgaapfcqegsprqssprcqggqggngggqqqkrmaigsgvllaadk
gyvvtnnhvvdnatvikvqlsdgrkfdakmvgkdprsdialiqiqnpknltaikmadsdal
rvgdytvaignpfglgetvtsgivsalgrsglnaenyenfiqtdaainrgnsggalvnlng
eligintailapdggnigigfaipsnmvknltsqmveygqvkrgelgimgtelnselakam
kvdaqrgafvsqvlpnssaakagikagdvitslngkpissfaalraqvgtmpvgskltlgl
lrdgkqvnvnlelqqssqnqvdsssifngiegaemsnkgkdqgvvvnnvktgtpaaqiglk
kgdviiganqqavkniaelrkvldskpsvlalniqrgdstiyllmq
```

Deg P of E. coli

Sequence 2 Enter accession or GI [Gilbert] or download from file [＿＿＿＿＿＿]
or sequence in FASTA format from: [＿＿＿] to: [＿＿＿]

```
mgikkvcicviciivrcrgiryrfarvnqqernavsilkakirneegkpvnilrcyciiqm
kvaerimaqhpgerfyvvlmsenrnekydyyfnqikdkaerayffylpyglnksfnfiptm
aelkvksmllpkvkriylaslekvsiaaflstypdaeiktfddgtnnliressylggefav
ngaikrnfarmmvgdwsiaktrnasdehytifkglknimddgrrkmtylplfdaselkagd
etggtvrillgspdkemkeisekaaknfniqyvaphprqtyglsgvtalnspyviedyilr
eikknphtryeiytffsgaaltmkdfpnvhvyalkpaslpedywlkpvyalfrqadipilt
fddkn
```

Gilbert
SEQ ID NO: 4

[Align] [Clear Input]

Blast 2 Sequences results

NCBI

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☑ Align

Sequence 1 lcl|seq_1 **Length** 473

Sequence 2 lcl|seq_2 **Length** 371

No significant similarity was found